International application No.

	· · · · · · · · · · · · · · · · · · ·			PCT/AU2004	/000919	
<b>A.</b> .	CLASSIFICATION OF SUBJECT MATT	ER				
Int. Cl. <sup>7</sup> :	C12N 15/12, C07K 14/47, A61K 38/1	7				
According to 1	International Patent Classification (IPC) or	to both r	national classification and IPC		•	
	FIELDS SEARCHED			<del></del>	· · · · · · · · · · · · · · · · · · ·	
Minimum docu	mentation searched (classification system follow	wed by cla	assification symbols)	· · · · · · · · · · · · · · · · · · ·		
			•	•	. •	
	searched other than minimum documentation to				hed	
Electronic data GenBank, El	base consulted during the international search (MBL, DDBJ and PDB (SEQ ID NO:1,	name of d	lata base and, where practicable, se DNO: 7, SEQ ID NO: 8)	earch terms used)		
C.	DOCUMENTS CONSIDERED TO BE RELEVE	VANT				
Category*	Citation of document, with indication, wl	here appi	ropriate, of the relevant passage	es	Relevant to claim No.	
х	GenBank database Accession Number AF461187.  Umeda, S; 'Macaca fascicularis ELOVL4 (ELOVL4) gene, exon 6 and complete cds.' 02-JAN-2003.  Nucleotide sequence is 76.4% identical to SEQ ID NO: 1 over 449 nucleotides as determined by Gap analysis					
X	GenBank database Accession Number AF277093.  Zhang, K., et al; 'Mus musculus Elovl4 mRNA, complete cds.' 12-JAN-2001  Nucleotide sequence is 81.5% identical to SEQ ID NO: 1 over 449 nucleotides as determined by Gap analysis					
GenBank database Accession Number U36188. Tsui, S. K. W., et al; 'Human clathrin assembly protein 50 (AP50) mRNA, complete cds.' 02-APR-1996. Nucleotide sequence is 92.8% identical to SEQ ID NO: 7 over 389 nucleotides as determined by Gap analysis						
X F	urther documents are listed in the cont	inuation	n of Box C X See p	atent family and	lex	
"A" docume	categories of cited documents: nt defining the general state of the art which is sidered to be of particular relevance pplication or patent but published on or after the	cc ui	ter document published after the internonflict with the application but cited to inderlying the invention	understand the princi	ple or theory	
internat	ional filing date	oi al	ocument of particular relevance; the clar cannot be considered to involve an in lone	ventive step when the	document is taken	
or which another	nt which may throw doubts on priority claim(s) h is cited to establish the publication date of citation or other special reason (as specified) nt referring to an oral disclosure, use, exhibition	in	ocument of particular relevance; the cla avolve an inventive step when the docu ach documents, such combination bein	ment is combined with	One or more other	
or other	means in published prior to the international filing date r than the priority date claimed	*&* de	ocument member of the same patent fa	mily		
Date of the act	ual completion of the international search er 2004		Date of mailing of the internation	onal search report	2 3 SEP 2004	
•	ling address of the ISA/AU		Authorized officer			
PO BOX 200, E-mail address	N PATENT OFFICE WODEN ACT 2606, AUSTRALIA :: pct@ipaustralia.gov.au (02) 6285 3929		Philippa Wyrdeman Telephone No: (02) 6283 25	554		

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C (Continuati	ion). DOCUMENTS CONSIDERED TO BE RELEVANT	
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to . claim No.
<b>X</b>	GenBank database Accession Number M23674.  Thurieau, C., et al; 'Rat assembly protein (AP50) associated with clathrin-coated vesicles mRNA, complete cds.' 12-AUG-1994.  Nucleotide sequence is 93.7% identical to SEQ ID NO: 7 over 389 nucleotides as determined by Gap analysis.	1 and 18
x	GenBank database Accession Number BC027103. Strausberg, R.; 'Mus musculus, clone MGC:38847 IMAGE:5360942, mRNA, complete cds.' 16-AUG-2002. Nucleotide sequence is 74.3% identical to SEQ ID NO: 8 over 781 nucleotides as determined by Gap analysis	1 and 18
x	GenBank database Accession Number AK046140. Carninci, P. and Hayashizaki, Y. 'Mus musculus adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone:B230344G04 product:hypothetical N-terminal nucleophile aminohydrolases (Ntn hydrolases) structure containing protein, full insert sequence.' 05-DEC-2002. Nucleotide sequence is 74.1% identical to SEQ ID NO: 8 over 781 nucleotides as determined by Gap analysis	1 and 18
х	WO 1999/023217; International Diabetes Institute; 14 MAY 1999.	1, 2, 8, 9, 18- 20, 26, 27 and 36-46
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Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)					
This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:					
1. Claims Nos.:					
because they relate to subject matter not required to be searched by this Authority, namely:					
· · · · · · · · · · · · · · · · · · ·					
2. X Claims Nos.: 42, 43 and 45					
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:					
The claims relate to agents capable of modulating AGT 711, AGT 717 and AGT 718, however, the claims do not specify what the agents are. These claims cannot be searched since the claims are not limited to any compound. Only those claims can be searched where one is able to determine if the compounds can act as					
modulating agents through a screening process.					
3. Claims Nos.:					
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a)					
Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)					
This International Searching Authority found multiple inventions in this international application, as follows:					
The ISA has identified 16 separate inventions.					
See attached sheet					
soo attached sheet					
1. As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.					
2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.					
3. X As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:					
1, 2, 8, 9, 18-20, 26, 27 and 36-46					
4. No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:					
Remark on Protest					
X No protest accompanied the payment of additional search fees.					

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### Supplemental Box

(To be used when the space in any of Boxes I to VIII is not sufficient)

Continuation of Box No: III

The claims are directed to nucleotide/polypeptide sequences that are differentially expressed in the hypothalamus, liver, red gastrocemius muscle and mesentric adipose tissue of lean animals, obese non-diabetic animals or obese diabetic animals.

The sequences have been found to be markers for conditions of healthy state, myopathy, obesity, anorexia, weight maintenance, diabetes, disorders associated with mitochondrial dysfunction, genetic disorders and metabolic energy levels. The sequences claimed appear to be involved in a large number of diseases (claim 41) and are either under or over expressed in the various tissues disclosed above in any particular group of animals.

Although all of the sequences share the feature that they are differentially expressed in lean, obese non-diabetic and obese diabetic animals, this does not represent a special technical feature.

This feature cannot be regarded as a special technical feature because it is not a feature that is representative of a single group of structurally or functionally related peptides or nucleic acids. In particular, the claimed sequences do not appear to represent a single class of genes or to share a significant level of homology.

Furthermore, given the nature of the claims and the invention, it is appropriate to apply the Markush approach. Using the Markush approach to analyse the unity of inventions, although the 16 sequences all have the common property that they are markers for conditions of healthy state, myopathy, obesity, anorexia, weight maintenance, diabetes, disorders associated with mitochondrial dysfunction, genetic disorders and metabolic energy levels, there is no common structure present in all of the sequences; and there is no single recognised class or group of compounds embracing all the sequences claimed. It is contrary to normal classification to group together such diverse sequences. Thus according to Markush, it is appropriate to classify the sequences in terms of the 16 individual groups and thus these groups represent 16 different inventions.

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### INTERNATIONAL SEARCH REPORT

Information on patent family members

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This Annex lists the known "A" publication level patent family members relating to the patent documents cited in the above-mentioned international search report. The Australian Patent Office is in no way liable for these particulars which are merely given for the purpose of information.

Patent Document Cited in Search Report		Patent Family Member							
wo	9923217	AU	10112/99	,	CA	2307839	EP	1030915	
	·	NZ	504327		NZ	520101	US	6436670	

Due to data integration issues this family listing may not include 10 digit Australian applications filed since May 2001.

**END OF ANNEX**